

SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana  
MacBeth, Kyle J.  
Williamson, Mark

<120> 22012, A Novel Human Carboxypeptidase

<130> 5800-38

<160> 4

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 492

<212> PRT

<213> Homo sapiens

<400> 1

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Arg Gly Leu Gln Ala Gly Ala Arg Arg Ala Pro Asp Pro Gly Phe Gln  
20 25 30  
Glu Arg Phe Phe Gln Gln Arg Leu Asp His Phe Asn Phe Glu Arg Phe  
35 40 45  
Gly Asn Lys Thr Phe Pro Gln Arg Phe Leu Val Ser Asp Arg Phe Trp  
50 55 60  
Val Arg Gly Glu Gly Pro Ile Phe Phe Tyr Thr Gly Asn Glu Gly Asp  
65 70 75 80  
Val Trp Ala Phe Ala Asn Asn Ser Gly Phe Val Ala Glu Leu Ala Ala  
85 90 95  
Glu Arg Gly Ala Leu Leu Val Phe Ala Glu His Arg Tyr Tyr Gly Lys  
100 105 110  
Ser Leu Pro Phe Gly Ala Gln Ser Thr Gln Arg Gly His Thr Glu Leu  
115 120 125  
Leu Thr Val Glu Gln Ala Leu Ala Asp Phe Ala Glu Leu Leu Arg Ala  
130 135 140  
Leu Arg Arg Asp Leu Gly Ala Gln Asp Ala Pro Ala Ile Ala Phe Gly  
145 150 155 160  
Gly Ser Tyr Gly Gly Met Leu Ser Ala Tyr Leu Arg Met Lys Tyr Pro  
165 170 175  
His Leu Val Ala Gly Ala Leu Ala Ala Ser Ala Pro Val Leu Ala Val  
180 185 190  
Ala Gly Leu Gly Asp Ser Asn Gln Phe Phe Arg Asp Val Thr Ala Asp  
195 200 205  
Phe Glu Gly Gln Ser Pro Lys Cys Thr Gln Gly Val Arg Glu Ala Phe  
210 215 220  
Arg Gln Ile Lys Asp Leu Phe Leu Gln Gly Ala Tyr Asp Thr Val Arg  
225 230 235 240  
Trp Glu Phe Gly Thr Cys Gln Pro Leu Ser Asp Glu Lys Asp Leu Thr  
245 250 255  
Gln Leu Phe Met Phe Ala Arg Asn Ala Phe Thr Val Leu Ala Met Met  
260 265 270  
Asp Tyr Pro Tyr Pro Thr Asp Phe Leu Gly Pro Leu Pro Ala Asn Pro

	275	280	285
Val Lys Val Gly Cys Asp Arg	Leu Leu Ser Glu Ala Gln Arg Ile Thr		
290	295	300	
Gly Leu Arg Ala Leu Ala Gly	Leu Val Tyr Asn Ala Ser Gly Ser Glu		
305	310	315	320
His Cys Tyr Asp Ile Tyr Arg	Leu Tyr His Ser Cys Ala Asp Pro Thr		
325	330	335	
Gly Cys Gly Thr Gly Pro Asp	Ala Arg Ala Trp Asp Tyr Gln Ala Cys		
340	345	350	
Thr Glu Ile Asn Leu Thr Phe	Ala Ser Asn Asn Val Thr Asp Met Phe		
355	360	365	
Pro Asp Leu Pro Phe Thr Asp	Glu Leu Arg Gln Arg Tyr Cys Leu Asp		
370	375	380	
Thr Trp Gly Val Trp Pro Arg	Pro Asp Trp Leu Leu Thr Ser Phe Trp		
385	390	395	400
Gly Gly Asp Leu Arg Ala Ala Ser Asn	Ile Ile Phe Ser Asn Gly Asn		
405	410	415	
Leu Asp Pro Trp Ala Gly Gly	Ile Arg Arg Asn Leu Ser Ala Ser		
420	425	430	
Val Ile Ala Val Thr Ile Gln	Gly Gly Ala His His Leu Asp Leu Arg		
435	440	445	
Ala Ser His Pro Glu Asp Pro	Ala Ser Val Val Glu Ala Arg Lys Leu		
450	455	460	
Glu Ala Thr Ile Ile Gly	Glu Trp Val Lys Ala Ala Arg Arg Glu Gln		
465	470	475	480
Gln Pro Ala Leu Arg Gly	Gly Pro Arg Leu Ser Leu		
485	490		

<210> 2  
<211> 1653  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> CDS  
<222> (19)...(1494)

<400> 2

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Met Gly Ser Ala Pro Trp Ala Pro Val Leu Leu  
1 5 10

51

ctg gcg ctc ggg ctg cgc ggc ctc cag gcg ggg gcc cgc agg gcc ccg  
 Leu Ala Leu Gly Leu Arg Gly Leu Gln Ala Gly Ala Arg Arg Arg Ala Pro  
 15 20 25

99

gac ccc ggc ttc cag gag cgc ttc ttc cag cag cgt ctg gac cac ttc  
 Asp Pro Gly Phe Gln Glu Arg Phe Phe Gln Gln Arg Leu Asp His Phe  
                  30                 35                 40

147

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aac ttc gag cgc ttc ggc aac aag acc ttc cct cag cgc ttc ctg gtg
Asn Phe Glu Arg Phe Gly Asn Lys Thr Phe Pro Gln Arg Phe Leu Val
        45           50           55

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195

tcg gac agg ttc tgg gtc cg<sup>g</sup> ggc gag ggg ccc atc ttc ttc tac act  
Ser Asp Arg Phe Trp Val Arg Gly Glu Gly Pro Ile Phe Phe Tyr Thr  
60 65 70 75

243

ggg aac gag ggc gac gtg tgg gcc ttc gcc aac aac tcg ggc ttc gtc Gly Asn Glu Gly Asp Val Trp Ala Phe Ala Asn Asn Ser Gly Phe Val 80 85 90	291
gct gag ctg gcg gcc gag cgg ggg gct cta ctg gtc ttc gct gag cac Ala Glu Leu Ala Ala Glu Arg Gly Ala Leu Leu Val Phe Ala Glu His 95 100 105	339
cgc tac tac ggg aag tcg ctg ccg ttc ggt gct cag tcc acg cag cgc Arg Tyr Tyr Gly Lys Ser Leu Pro Phe Gly Ala Gln Ser Thr Gln Arg 110 115 120	387
ggg cac acg gag ctg ctg acg gtg gag cag gcc ctg gcc gac ttc gca Gly His Thr Glu Leu Leu Thr Val Glu Gln Ala Leu Ala Asp Phe Ala 125 130 135	435
gag ctg ctc cgc gcg cta cga cgc gac ctc ggg gcc cag gat gcc ccc Glu Leu Leu Arg Ala Leu Arg Arg Asp Leu Gly Ala Gln Asp Ala Pro 140 145 150 155	483
gcc atc gcc ttc ggt gga agt tat ggg ggg atg ctc agt gcc tac ctg Ala Ile Ala Phe Gly Gly Ser Tyr Gly Gly Met Leu Ser Ala Tyr Leu 160 165 170	531
agg atg aag tat ccc cac ctg gtg gcg ggg gcg ctg gcg gcc agc gcg Arg Met Lys Tyr Pro His Leu Val Ala Gly Ala Leu Ala Ala Ser Ala 175 180 185	579
ccc gtt cta gct gtg gca ggc ctc ggc gac tcc aac cag ttc ttc cgg Pro Val Leu Ala Val Ala Gly Leu Gly Asp Ser Asn Gln Phe Phe Arg 190 195 200	627
gac gtc acg gcg gac ttt gag ggc cag agt ccc aaa tgc acc cag ggt Asp Val Thr Ala Asp Phe Glu Gly Gln Ser Pro Lys Cys Thr Gln Gly 205 210 215	675
gtg cgg gaa gcg ttc cga cag atc aag gac ttg ttc cta cag gga gcc Val Arg Glu Ala Phe Arg Gln Ile Lys Asp Leu Phe Leu Gln Gly Ala 220 225 230 235	723
tac gac acg gtc cgc tgg gag ttc ggc acc tgc cag ccc ctg tca gac Tyr Asp Thr Val Arg Trp Glu Phe Gly Thr Cys Gln Pro Leu Ser Asp 240 245 250	771
gag aag gac ctg acc cag ctc ttc atg ttc gcc cgg aat gcc ttc acc Glu Lys Asp Leu Thr Gln Leu Phe Met Phe Ala Arg Asn Ala Phe Thr 255 260 265	819
gtg ctg gcc atg atg gac tac ccc act gac ttc ctg ggt ccc Val Leu Ala Met Met Asp Tyr Pro Tyr Pro Thr Asp Phe Leu Gly Pro 270 275 280	867
ctc cct gcc aac ccc gtc aag gtg ggc tgt gat cgg ctg ctg agt gag Leu Pro Ala Asn Pro Val Lys Val Gly Cys Asp Arg Leu Leu Ser Glu 285 290 295	915

gcc cag agg atc acg ggg ctg cga gca ctg gca ggg ctg gtc tac aac Ala Gln Arg Ile Thr Gly Leu Arg Ala Leu Ala Gly Leu Val Tyr Asn 300 305 310 315	963
gcc tcg ggc tcc gag cac tgc tac gac atc tac cggtc tac cac agc Ala Ser Gly Ser Glu His Cys Tyr Asp Ile Tyr Arg Leu Tyr His Ser 320 325 330	1011
tgt gct gac ccc act ggc tgc ggc acc ggc ccc gac gcc agg gcc tgg Cys Ala Asp Pro Thr Gly Cys Gly Thr Gly Pro Asp Ala Arg Ala Trp 335 340 345	1059
gac tac cag gcc tgc acc gag atc aac ctg acc ttc gcc agc aac aat Asp Tyr Gln Ala Cys Thr Glu Ile Asn Leu Thr Phe Ala Ser Asn Asn 350 355 360	1107
gtg acc gat atg ttc ccc gac ctg ccc ttc act gac gag ctc cgc cag Val Thr Asp Met Phe Pro Asp Leu Pro Phe Thr Asp Glu Leu Arg Gln 365 370 375	1155
cgg tac tgc ctg gac acc tgg ggc gtg tgg ccc cgg ccc gac tgg ctg Arg Tyr Cys Leu Asp Thr Trp Gly Val Trp Pro Arg Pro Asp Trp Leu 380 385 390 395	1203
ctg acc agc ttc tgg ggg ggt gat ctc aga gcc gcc agc aac atc atc Leu Thr Ser Phe Trp Gly Asp Leu Arg Ala Ala Ser Asn Ile Ile 400 405 410	1251
ttc tcc aac ggg aac ctg gac ccc tgg gca ggg ggc ggg att cgg agg Phe Ser Asn Gly Asn Leu Asp Pro Trp Ala Gly Gly Ile Arg Arg 415 420 425	1299
aac ctg agt gcc tca gtc atc gcc gtc acc atc cag ggg gga gcg cac Asn Leu Ser Ala Ser Val Ile Ala Val Thr Ile Gln Gly Gly Ala His 430 435 440	1347
cac ctc gac ctc aga gcc tcc cac cca gaa gat cct gct tcc gtg gtt His Leu Asp Leu Arg Ala Ser His Pro Glu Asp Pro Ala Ser Val Val 445 450 455	1395
gag gcg cgg aag ctg gag gcc acc atc atc ggc gag tgg gta aag gca Glu Ala Arg Lys Leu Glu Ala Thr Ile Ile Gly Glu Trp Val Lys Ala 460 465 470 475	1443
gcc agg cgt gag cag cag cca gct ctg cgt ggg ggg ccc aga ctc agc Ala Arg Arg Glu Gln Gln Pro Ala Leu Arg Gly Gly Pro Arg Leu Ser 480 485 490	1491
ctc tgagcacagg actggagggg tctcaaggct cctcatggag tgggggcttc Leu	1544
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<210> 3  
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<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence for the prolyl oligopeptidase family from the Prosite database of protein patterns

<400> 3

Ile Phe Gly Gly Ser Asn Gly Gly Leu Leu  
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<210> 4

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence for the alpha/beta hydrolase family from the Prosite database of protein patterns

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Pro Ser Asp Leu Ala Asp Tyr Arg Phe Asp Asp Leu Ala Glu Asp Leu  
20 25 30  
Glu Ala Leu Leu Asp Ala Leu Gly Leu Asp Lys Pro Val Ile Leu Val  
35 40 45  
Gly His Ser Met Gly Gly Ala Leu Ala Ala Ala Tyr Ala Ala Lys Tyr  
50 55 60  
Pro Glu Glu Arg Val Lys Ala Leu Val Leu Val Ser Thr Pro Ala Pro  
65 70 75 80  
Ala Gly Leu Ser Ser Arg Leu Phe Pro Arg Leu Gly Asn Leu Glu Gly  
85 90 95  
Leu Leu Leu Ala Asn Phe Phe Asn Arg Leu Ser Arg Ser Val Glu Ala  
100 105 110  
Leu Leu Gly Arg Ala Leu Lys Gln Phe Phe Leu Leu Gly Arg Pro Phe  
115 120 125  
Val Ser Asp Phe Leu Lys Gln Ala Glu Asp Trp Leu Ser Ser Leu Ala  
130 135 140  
Arg Pro Gly Glu Thr Asp Gly Gly Asp Gly Leu Leu Gly Tyr Ala Val  
145 150 155 160  
Ala Leu Gly Lys Leu Leu Gln Trp Asp Arg Ser Ala Leu Lys Asp Ile  
165 170 175  
Lys Val Pro Thr Leu Val Ile Trp Gly Asp Asp Asp Pro Leu Val Pro  
180 185 190  
Leu Lys Ala Ser Glu Lys Leu Ser Ala Leu Phe Pro Asn Ala Glu Val  
195 200 205  
Val Val Ile Asp Asp Ala Gly His Leu Ala Leu Leu Glu Lys Pro Glu  
210 215 220  
Glu Val Ala Glu Leu Ile Lys Phe Leu Ala Leu Ser Thr Asn Asx Ile  
225 230 235 240  
Arg Asp Ala Leu Ser Thr Asn Asx Ile Arg Asp  
245 250